

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 23, 2001, 14:19:05 ; Search time 11.78:seconds

(without alignments)  
1279.492 Million cell updates/sec

Title: US-08-883-036A-2

Perfect score: 2327

Sequence: 1 MEORGQNPAPASGARRKRP.....HLSSGKFMYLEGNADSAMS 440

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues 93435.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271.5	11.7	471	1	TNRI_BOVIN
2	243	10.4	461	1	TNRI_PIG
3	218	9.4	454	1	TNRI_MOUSE
4	215	9.2	455	1	TNRI_HUMAN
5	209	9.0	435	1	TNRC_HUMAN
6	203.5	8.7	417	1	WSL1_HUMAN
7	197	8.5	335	1	FASA_HUMAN
8	179.5	7.7	327	1	FASA_MOUSE
9	176.5	7.6	323	1	FASA_BOVIN
10	173.5	7.5	461	1	TNRI_RAT
11	172	7.4	461	1	TNRI_HUMAN
12	170.5	7.3	332	1	FASA_PIG
13	169.5	7.3	415	1	TNRC_MOUSE
14	166	7.1	427	1	NGFR_HUMAN
15	163.5	7.0	474	1	TNRI_MOUSE
16	161.5	6.9	416	1	NGFR_CHICK
17	155	6.7	425	1	NGFR_RAT
18	148.5	6.4	324	1	FASA_RAT
19	142	6.1	272	1	OX40_MOUSE
20	141	6.1	349	1	VC22_VARV
21	139.5	6.0	595	1	CD30_HUMAN
22	137	5.9	271	1	OX40_RAT
23	136.5	5.9	277	1	CD40_HUMAN
24	131.5	5.7	577	1	TBRM_MOUSE
25	131	5.6	2813	1	VWF_CANFA
26	129.5	5.6	277	1	OX40_HUMAN
27	128	5.5	326	1	VT2_MXVL
28	126.5	5.4	519	1	ERR1_HUMAN
29	126	5.4	256	1	41BB_MOUSE
30	122	5.2	462	1	ERR1_MOUSE
31	120	5.2	1808	1	TENA_CHICK
32	118.5	5.1	289	1	CD40_MOUSE
33	118.5	5.1	356	1	TBRM_BOVIN

34	116.5	5.0	575	1	TBRM_HUMAN
35	116	5.0	976	1	EPAL_HUMAN
36	113	4.9	325	1	VT2_SEVKA
37	112	4.8	1436	1	WC11_BOVIN
38	111.5	4.8	667	1	TS11_GITALA
39	110.5	4.7	655	1	HGRA_HUMAN
40	110.5	4.7	1877	1	PCRS_MOUSE
41	110.5	4.7	2482	1	VWF_PIG
42	110	4.7	250	1	CD27_MOUSE
43	110	4.7	1696	1	PKC5_BRACL
44	109	4.7	2201	1	TENA_HUMAN
45	108.5	4.7	1323	1	LT23_CAEL

## ALIGNMENTS

RESULT 1

ID	TNRI_BOVIN	STANDARD	PRT	471 AA.
AC	019131;			
DT	01-OCT-2000 (Rel. 40, Created)			
DT	01-OCT-2000 (Rel. 40, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI)			
DE	(P55).			
GN	TNFRSF1A OR TNFRI.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Arteria;			
RA	Lee E.-K., Talyor M.J., Kehli M.E.;			
RT	"Cloning of cDNA encoding bovine tumor necrosis factor-receptor 1			
RT	(TNF-RI).";			
RT	Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD			
CC	RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING			
CC	AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)			
CC	PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE			
CC	SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE			
CC	PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).			
CC	- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS TO			
CC	HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS			
CC	PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY			
CC	WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING			
CC	PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO			
CC	TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX			
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND			
CC	NF-KAPPA B SIGNALING (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: U90937; AAB65143.1; -			
DR	HSSP: P19438; 1TNR.			
DR	InterPro: IPR000488; -			
DR	InterPro: IPR001368; -			
DR	Pfam: PF00020; TNFR.c6; 3.			
DR	Pfam: PF00531; death; 1.			
DR	PROSITE: PS00652; TNFR_NGFR_1; 3.			
DR	PROSITE: PS00500; TNFR_NGFR_2; 2.			

DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
 FT SIGNAL 1 21  
 FT CHAIN 22 471  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 471  
 FT DOMAIN 43 195  
 FT REPEAT 83 82  
 FT REPEAT 126 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 360  
 FT DOMAIN 372 457  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 190  
 FT DISULFID 185 194  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 471 AA; 51367 MW; 5243E51ADBE81C4 CRC64;

Query Match 11.7%; Score 271.5; DB 1; Length 471;  
 Best Local Similarity 25.2%; Pred No. 4.5e-12;  
 Matches 121; Conservative 59; Mismatches 198; Indels 103; Gaps 25;

32 PRVPTLVVAVALLL-----VSASALITOODLAPQRAAPQOKRSPSEGL-----CP 82  
 4 PIVPGLLEPLVLPALLADYYPAGVGLVPHGDLERKSPQGNHNPONSTICCTKCH 63  
 83 PGNHISED-----GR--DCISCKYGDYSTHWNDLFLCLCTRC--DSGEVELSPCTTTN 134  
 64 KQTYLYNDPCPGGRDTCWYCAPG--TYTALENHLRCLSCSRCDMPFVYELSPCVVDRD 122  
 135 TVCOCEEGTFRE--EDSPMCRKCRTPGRCWYKVDCTPMWSDIECVHESG-----184  
 123 TVCGCRKNQYREYWGEGTGRCLNCSL--CPNGIVNT--PCQERDPTIC--HGMGFPLKGARC 179  
 185 -TRHSGEAPAVEETVTSPT-----PASPCSLGIII--GVVAVALVIVAVCKSL 236  
 180 ISCHDCKNKECKLCTPTBSTGKDSODPCTVLLPLVIFGLCLASFASV--VLACRYOR 237  
 237 WKKVLPYLKIGISGGG-----GDPEVNDVS-----SORPAEDVLEIVS---277  
 238 WK--PKYLSIIICGSLVKESEPELVAPGFNPPTTICFSTBSSSVSIPPYISCDR 294  
 278 -----ILOPTQV-----PEQEMEVQEPAEPTGVNMLSPG--ESEHLEPAE 316  
 295 SMFGAVASPSSETAPRHLKAGPILPGPASTHLCTPGPASTHLCTPGPASTHLCTPQ 354  
 317 AERSORRLLVANECDPTETLRQCFDDPADLVPEDSWEPLMKLGMLDNEIKVAKAENA 376  
 355 KWEASAPAPDOLADADPA--TLYAVVDG---VPSRMKELVRRLGLSHEIERLENG 409  
 377 GH--RDTLYMLIKWVNT-----GRDASVHTLDALETIGERL--AKQKIEDHL 422  
 410 RLRLRAQYSMLAAMRRKRPREATLELLGRVLRDMDLGCLLENIEBALGGAARLASEPRL 469  
 423 L 423  
 470 L 470

RESULT 2  
 ID TNRL\_PIG STANDARD; PRT: 461 AA.  
 AC P50555;  
 DT 01-OCT-1996 (rel. 34, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 01-OCT-2000 (rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55)  
 DE (P55)  
 GN TNFRSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxId=9823;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT \*Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
 RL Gene 163:263-266(1995).  
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: U19994; AAC48499.1; -  
 DR HSSP: P19438; 1TNR.  
 DR InterPro: IPR000488; -  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR Pfam: PF00531; death\_1.  
 DR DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 2.  
 DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
 FT SIGNAL 1 21  
 FT CHAIN 22 461  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 461  
 FT DOMAIN 43 195  
 FT REPEAT 83 82  
 FT REPEAT 126 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 350  
 FT DOMAIN 362 447  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81

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FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 190 BY SIMILARITY.
FT DISULFID 185 194 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA: 50696 MW: CD72361EC60C9D43 CRC64;

Query Match 10.48; Score 243; DB 1; Length 461;
Best Local Similarity 24.68; Pred. No. 4.4e-10;
Matches 119; Conservative 61; Mismatches 185; Indels 118; Gaps 26;

OY 30 PGPRVKTLYVVAAYLLV---SASALITQODLAPQORAAQOKRSSPSE-----GLC 81
DB 7 PGLLP-----LVRLALVDVYPAGVGHVLPDREKRESLCQKYSHPQNSICTK 62
OY 82 PGCHISED-----GRDCISCKYGODYSTHNDLFCULCTRCDS--GEVELSPCTTTR 133
DB 63 HKGTYLHNDCLGFLDPTDCRECDNG--TFPASENHLTQCLSCSKCRSEMSQVEISPCVDR 121
OY 134 NTYCQCEEGFREDSPEM--CRKCRGCRGVKVGDCIPASD----- 175
DB 122 DTVCGGRKNQYRWSETLFQCLNCSL--CPNGTVOL--PCLEKODITONCHSGFFLDKEC 179
OY 176 IECVH-KESGTRKSGEPAVEETVTSPTGPASPCSLGIIIGVVAAYVLIYAVFCVS 234
DB 180 VSCVGNKAKMDCKNL--CPATSETRANDPQDTGTVLLPLVFFELCLAFLEFV--GLACRY 235
OY 235 LMKKVLPLYLKIGSGG-----GDEPERVDRS-----SORPAEDNVLINEIV 276
DB 236 QRWK---PKLYSTICKSPVKEGEPEPLATAPSPITFTSPISFSPPTTSSPVPSFS 292
OY 277 SLIQPTQVP--EDEMVOEPAE-----PTGVNMLSP-----GSEHLLEP 314
DB 293 PISPFPTPDMSNIRYVTSPPKEIAPPGAGPILMPASTVPVPTPLPKMGSAHSAHS 352
OY 315 AEAEERQORRLVPAWEGDPTETLRQCFDPAFLPESDESMELRKLGLMDNET--VYAKA 373
DB 353 APQOLA-----DADPA--TLVAVNDG---VPPTKKEVYKRLGISEHETLELQ 397
OY 374 EAAGHRDLYMLIKWVNTG--RDASVH-----TLDALETIGERL--AKOKIED 420
DB 398 NGRCLEAGYSMLAEWRRTSRREATLELLGSLVLRMDLLGCLLEIEALRGPARLAPAP 457
OY 421 HLL 423
DB 458 HLL 460

RESULT 3
TNRI_MOUSE STANDARD: PRT: 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)
DE (P55).
DE TNFRSF1A OR TNFR1 OR TNFR-1.
OS GN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE-91187885; PubMed-1849278;
RX Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RX Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RX MEDLINE-91246168; PubMed-1645445;
RX Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,
RX Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RT Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RX MEDLINE-91285014; PubMed-1647956;
RX Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
RX Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55
RT tumor necrosis factor receptor."
RT Eur. J. Immunol. 21:1649-1656(1991).
RN [4]
RX SEQUENCE FROM N.A.
RX TISSUE-Spleen;
RX MEDLINE-92039815; PubMed-1657766;
RX Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT "Molecular cloning and expression of the mouse Tnf receptor type b."
RT Immunogenetics 34:338-340(1991).
RN [5]
RX SEQUENCE FROM N.A.
RX MEDLINE-94245292; PubMed-8188324;
RX Bebo B.F., Linthicum D.S.;
RT "Nucleotide sequence of the TNF type I receptor from a mouse
RT endothelioma cell line."
RT Immunogenetics 39:450-451(1994).
RN [6]
RX SEQUENCE FROM N.A.
RX MEDLINE-93156721; PubMed-8381516;
RX Rothe J., Bluethmann H., Gentz R., Lesslauer W., Stelmets M.;
RT "Genomic organization and promoter function of the murine tumor
RT necrosis factor receptor beta gene."
RT Mol. Immunol. 30:165-175(1993).
RN [7]
RX FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
RX AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
RX PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
RX SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
RX PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
RN [8]
RX SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
RX HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
RX PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
RX WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
RX PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
RX TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
RX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
RX NF-KAPPA B SIGNALING (BY SIMILARITY).
RN [9]
RX SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
RX -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
RX -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
RN [10]
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RX or send an email to license@isb-sib.ch).
RN [11]
RX EMBL: M60468; AAA39751.1; -
RX EMBL: M59377; AAA40464.1; -
RX EMBL: X59238; CAA41922.1; -

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DR EMBL: X57796; CAA40936.1; -
DR EMBL: L26349; AAA59361.1; -
DR EMBL: M76556; AAA40465.1; -
DR EMBL: M8067; AAA40465.1; JOINED.
DR EMBL: M7655; AAA40465.1; JOINED.
DR PIR: A3634; GOMST1.
DR PIR: S1677; S1677.
DR PIR: S19021; S19021.
DR HSSP: P19438; TEXT.
DR MGD: MGI:131484; Tnfstfla.
DR InterPro: IPR000488; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_c6; 4.
DR PROSITE: PS00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
KW SIGNAL.
FT CHAIN 1 21
FT SIGNAL 1 21
FT CHAIN 22 454
FT SIGNAL 22 454
FT TRANSMEM 22 212
FT TRANSMEM 213 235
FT DOMAIN 236 454
FT DOMAIN 43 196
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 339 349
FT DOMAIN 356 441
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHD 54 54
FT CARBOHD 151 151
FT CARBOHD 202 202
FT CONFLICT 394 394
SQ SEQUENCE 454 AA; 50129 MM; 0710C2E8C3C2B6D9 CRC64;

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Query Match 9.4%; Score 218; DB 1; Length 454;
Best Local Similarity 22.2%; Pred. No. 2.5e-08;
Matches 109; Conservative 51; Mismatches 163; Indels 168; Gaps 22;
OY 32 PVPPTLVVVAVALLLVSAESALITQODLAPOQRAAPQOKSSPSEGLCPGHHI----- 87
DB 4 PVPPELLSLVALLALMLGHPGVS---TGLVPS--LGDKEKDS---LCPKGVVSHSKN 54
OY 88 -----SEDGRD--CISCKYGDYSTHMDLFLCLNCTRC--DSGEVE 125
DB 55 NSICCTCKHKGTYLVSDPSGRDITVCRECKG--FTFASQNLRLGCLSCIKCRKMSQVE 113
OY 126 LSPCTTTNTNYOQCEGIFREDSPDM-----CRKCRFG-----CPRG-M 164
DB 114 ISPCGADKDYOGCKENOFYRLSTHFQCYDCCSPCFNGTYVTPCKETQNTVCNCHAGFF 173
OY 165 VKVGDCPTMSDIECVHKSSTGRKHSGEAPAVEETVSSPGTASPCSLGIIIGVVAVV 224
DB 174 LRESGVCS--HCKKNECKMLCLPPLAVNTNPDSGTAV---LPLVLGLGLLS 227
OY 225 LIVAVVCKSLMKKVLRYLKGICSGGGDEPVRDSSRQGAEDNVNLEIVSILOPTOV 284
DB 228 FIFISLMCRYFRW-----RP-----EYYSITICRPV 253

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OY 285 PROEMEVQEPAP-----TGVN-----MISPESE-----HLEPA 315
DB 254 PVKEERAGPLTPAPSPAPSPSTSGFNPLTGSTPGSSSVSTPISPLFGPSNMHPMPV 313
OY 316 EARSQRRLVLANEGD-----PTFLRCQFDFA-----DL 348
DB 314 SE-----VPTGQADLLTESLCSVPAPTSYQCKWESAHQRPDNDALILYAVDG 365
OY 349 VPPDSWEPMLKRLGMDNEI-KVAKAEAGHDTLYMLIKVNTKGDASYHTLLDALE 407
DB 366 VPPARKKEFRFMGLSEHIEERLEMQNGRCLEAGYSMLLEAWRRRTPRHE-----DTLE 419
OY 408 TLGERLAKOKI 418
DB 420 VVGLVLSKMLL 430

RESULT 4
TNRL_HUMAN STANDARD: PRT: 455 AA.
AC P19438;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
GN BINDING PROTEIN 1) (TNFRI) (P60) (TNF-RI) (P55) (CD120A).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Placenta;
RC MEDLINE=90235285; PubMed=2158863;
RX Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lenz R., Raab H., Kohn W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RL Cell 61:361-370(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RL factor receptor.";
RL Cell 61:351-359(1990).
RN [3]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE=91006021; PubMed=1698610;
RA Nopar Y., Kemper O., Brakebusch C., Engelmann H., Zhang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL EMBO J. 9:3269-3278(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Foy I., Kroenke M., Scheurich P., Pflizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [5]
RP SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=91017509; PubMed=2170974;
RA Gray P.W., Barrett K., Chantley D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and

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RT expression of recombinant soluble TNF-binding protein.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
 RL [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92250049; PubMed-1315717;  
 RA Fuchs P., Strehl S., Dworzak M., Hummler A., Ambros P.F.,  
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 RL localization to chromosome 12p13.";  
 RN Genomics 13:219-224(1992).  
 RP [7]  
 RX SEQUENCE OF 41-45.  
 RA MEDLINE-90110215; PubMed-2153136;  
 RT Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE-93358809; PubMed-8387891;  
 RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
 RT Broger C., Loetscher H., Lesslauer W.;  
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 RT beta complex: implications for TNF receptor activation.";  
 RL Cell 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE-97094982; PubMed-8939750;  
 RA Nalimath J.H., Devine T.O., Khono H., Sprang S.R.;  
 RT "Structures of the extracellular domain of the type I tumor necrosis  
 RT factor receptor.";  
 RL Structure 4:1251-1262(1996).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF  
 CC NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION  
 CC OF THE ACID SPHINGOMYELINASE.  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120a entry;  
 CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".  
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 CC -----  
 CC EMBL; X55313; CAA39021.1; -  
 CC EMBL; M33294; AAA03210.1; -  
 CC EMBL; M58286; AAA36753.1; -  
 CC EMBL; M63121; AAA36754.1; -  
 CC EMBL; M75866; AAA61201.1; -  
 CC EMBL; M75866; AAA61201.1; -  
 CC EMBL; M75866; AAA61201.1; JOINED.  
 CC EMBL; M75865; AAA61201.1; JOINED.  
 CC EMBL; M60275; AAA36756.1; -

DR EMBL; A21522; CAA01556.1; -  
 DR PIR; A34899; GQHU11.  
 DR PIR; A35010; A35010.  
 DR PIR; S12057; S12057.  
 DR PIR; A38208; A38208.  
 DR PDB; 1TNR; 31-JUL-94.  
 DR PDB; 1NCF; 07-DEC-95.  
 DR PDB; 1EXT; 11-JAN-97.  
 DR MIM; 191190; -  
 DR InterPro; IPR000488; -  
 DR InterPro; IPR001368; -  
 DR Pfam; PF000020; TNFR\_C6; 4.  
 DR Pfam; PF00531; death; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;  
 KW 3D-structure; 1  
 FT SIGNAL 22 455  
 FT CHAIN 41 291  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 455  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 338 348  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 FT CONFLICT 412 412  
 FT CONFLICT 443 446  
 SQ SEQUENCE 455 AA; 50494 MW; 4CEBBA96D03B8225 CRC64;  
 Query Match 9.2%; Score 215; DB 1; Length 455;  
 Best Local Similarity 23.0%; Pred. 4.1e-08;  
 Matches 109; Conservative 62; Mismatches 172; Indels 130; Gaps 22;  
 QY 34 VPTLVVVAVALVLLVSAESALITQODLAPQORAPQOKRSPSEGLCPGHIIHSEDR- 92  
 DB 6 VPDLRLPLVLELLVGVIPSGVI---GLVP--HLGDEKEDS---YCPGKIYHPQNS 56  
 QY 93 -----DCISCKYGDYSTHWNDLFLCLRTCR--DSGEVELS 127  
 DB 57 ICSTKCHKGTLYLNDGPGQDIDCRCEESG-SFTASENHLRHLCSCKRKEGVEIS 115  
 QY 128 PCTTTRNTVQCEGEGTREDSPEM--CRKCRGCPRGWVKVDCPQWSDIECVHRSRG- 184  
 DB 116 SCVYDRDTVCGRKNQNRHYWSENLEFCFNCSL-CLNGTV-----HLSCQKQNTV 165  
 QY 185 -TKHSGEAPAVEETVTSPPCTPAPC-----SLSGIIGVTVAAVVLIVAVFC-R 233  
 DB 166 CTCHAGFFLENNCSNCKKSLCTKTLCLPQIENAVKGTEDSGTYLLPLVIFFGCLL 225  
 QY 234 SL-----WKVLPYLKIGICSGGGDPER--VDRSSORPGAEADVLEIYSILO 280

DB 226 SLF1GLMYRYOKRMSKXISI--VC--GKSTPEKEGELESTTTKPLAPNPSFSP-----T 276  
 QY 281 PQGVPEQMEVQAPAPPTGVNMLSPGESEHLLPAPAEBSQRRLVPAPEG----- 332  
 DB 277 PGTPPLGSPVPSSTFTSSSTYTPGDCPFAAP-----RREVAAPYOGADPILATA 328  
 QY 333 ---DPTETLRQCFDPA-----DLVPEDSWEPMLRKLGLMDNEI-KV 370  
 DB 329 LASDPIPNPLQKWEBSAHKQSLDTPATLAVAVENVPRLMKKEFVRRRLGSLDHEIDL 388  
 QY 371 AKAAGAAGHDLYTLMLIKVYKNT-----GRDASVHTLLDALETGERL 413  
 DB 389 ELONGRCLEBAQYSMLATWRRTTREPAREATLELLGRVLRMDMLGCEDEIDEAL 441

RESULT 5  
 TNRC\_HUMAN  
 ID TNRC\_HUMAN STANDARD: PRT; 435 AA.  
 AC P36941;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR  
 DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).  
 GN LTRB OR TNFR OR TNFRSF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=9325381; PubMed=8486360;  
 RA Baens M., Chaffanet M., Cassiman J.J., den Bergh H., Marynen P.,  
 RT "Construction and evaluation of a hncDNA library of human 12p  
 RT transcribed sequences derived from a somatic cell hybrid."  
 RL Genomics 16:214-218(1993).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=9422509; PubMed=8171323;  
 RX Crowe P.D., van Asdale T.L., Walter B.N., Ware C.F., Hession C.,  
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
 RT "A lymphotoxin-beta-specific receptor."  
 RL Science 264:707-710(1994).  
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC  
 CC EMBL: I04270; AAA36757.1; -  
 CC HSSP: P25942; ICDF.  
 DR DR  
 DR MIM: 600979; -  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 435  
 FT DOMAIN 31 227 LYMPHOTOXIN-BETA RECEPTOR.  
 FT TRANSMEM 228 248 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 249 435 POTENTIAL.  
 FT DOMAIN 42 211 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 42 81 4 X TNFR-CYS.  
 FT REPEAT 82 124 TNFR-CYS 2.

FT REPEAT 125 168 TNFR-CYS 3.  
 FT REPEAT 169 211 TNFR-CYS 4.  
 FT DISULFID 43 58 BY SIMILARITY.  
 FT DISULFID 59 72 BY SIMILARITY.  
 FT DISULFID 62 80 BY SIMILARITY.  
 FT DISULFID 83 98 BY SIMILARITY.  
 FT DISULFID 101 116 BY SIMILARITY.  
 FT DISULFID 104 124 BY SIMILARITY.  
 FT DISULFID 126 132 BY SIMILARITY.  
 FT DISULFID 139 148 BY SIMILARITY.  
 FT DISULFID 142 167 BY SIMILARITY.  
 FT DISULFID 170 185 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 435 AA; 46709 MW; 624626b6022f56f CRC64;

Query Match 9.0%; Score 209; DB 1; Length 435;  
 Best Local Similarity 24.5%; Pred. No. 1e-07;  
 Matches 91; Conservative 39; Mismatches 129; Indels 112; Gaps 18;

QY 20 PGPREARGARPGPRVKTLYVVAVALIVSAESALITQODLAPQORAPQOKRSSPSE- 78  
 DB 4 PWATSAFGLAMGP-----LVGLFGLAA-----SOPQAVPPYASENQTCRQDEKEY 50  
 QY 79 -----GLCPGHHISEDG--RD--CISCKYQDSTYHNDLLFCLRCTCD--SG 122  
 DB 51 YEPQHRICSSRCPGTYVSAKSRINDYCATCA-ENSYNEHMYNTLITCOLRCPDPMVG 109  
 QY 123 EVELSPCTTTRNTVCCCESTFREEDSPKCRKCRGCRGAKYVQDCTPMQDIE----- 177  
 DB 110 LERDIAPCTSRKTKQCCRCQGMFCAMALE-CTHCEL-----LSDCPGTEAELEKDEV 160  
 QY 178 -----CVKESGCTKSGEAPAV-----EETVTSPPGTPAS-----PCS 210  
 DB 161 GKGNHNCVCKAGHPONTSPSPARCPHTRCENQGLVEAPGAGSDITCKNPLEPPE 220  
 QY 211 LSGIIGVTY---AAVLIVAVFVCKSLWK-----KVLPLYKIGCGGGGDERVD 259  
 DB 221 MSGTMLMLAVLLPLAFELLAVFSC--IMKSHPSLCKRLKSLKRRQGEQPNV--- 274  
 QY 260 RSSQRGAEVDNNEIVSLIPLQ-----VPEQMEVQAPAPPTGV 300  
 DB 275 AGSWEPKAPHPYFPLDPLPSGDSVSPSTGLPAPVLEAGVPOQ---OSPDLTRE 330  
 QY 301 NMLSPGESEHL 311  
 DB 331 POLPEGEQSOV 341

RESULT 6  
 WSL\_HUMAN  
 ID WSL\_HUMAN STANDARD: PRT; 417 AA.  
 AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;  
 AC Q99830;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-  
 DE (APOPTOSIS INDUCING TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)  
 DE RECEPTOR OF DEATH) (LARD).  
 GN TNFRSF12 OR WSL OR APO3 OR DR3 OR DR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.  
 RC TISSUE=Lymphoid;  
 RX MEDLINE=97088617; PubMed=8934525;  
 RX Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
 RA Grlham C.J., Brown R., Farrow S.N.;

RT "A death-domain-containing receptor that mediates apoptosis.";  
 RL Nature 384:372-375(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=umbilical vein endothelial cells;  
 RX MEDLINE=97081063; PubMed=8875942;  
 RA Chinaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
 Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
 RT "Signal transduction by DR3, a death domain-containing receptor  
 related to TNFR-1 and CD95.";  
 RL Science 274:990-992(1996).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBD databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=97148200; PubMed=8994832;  
 RA Masters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
 Goddard A.D., Bauer K.D., Ashkenazi A.;  
 RT "Ap-3, a new member of the tumor necrosis factor receptor family,  
 contains a death domain and activates apoptosis and NF-kappa-B.";  
 RL Curr. Biol. 6:1669-1676(1996).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97272273; PubMed=9114039;  
 RA Sreteron G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,  
 McMichael A.J., Bell J.T.;  
 RT "LARD: a new lymphoid-specific death domain containing receptor  
 regulated by alternative pre-mRNA splicing.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 [6]  
 RP SEQUENCE OF 4-417 FROM N.A.  
 RC TISSUE=Brain, and Fetal Lung;  
 RX MEDLINE=97205335; PubMed=9052839;  
 RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Stehner V.,  
 Thome M., Bornand T., Hahne H.R., Tschopp J.;  
 RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology  
 to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)."  
 RL Immunity 6:79-88(1997).  
 [7]  
 RP SEQUENCE OF 7-417 FROM N.A.  
 RC TISSUE=Brain;  
 RA Chaudhary P.M., Hood L.E.;  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBD databases.  
 CC -1- FUNCTION: INDICES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B  
 (NF-KAPPA-B). DIRECTLY INTERACTS WITH TRADD ADAPTOR MOLECULE. MAY  
 PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.  
 CC -1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH  
 THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO  
 ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 NF-KAPPA-B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: WSL-1/LARD-1A (SHOWN HERE),  
 WSL-S/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND  
 LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,  
 COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.  
 CC -1- PTM: GLYCOSYLATED (PROBABLE).  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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 CC EMBL; Y09392; CAA70561.1; -

DR EMBL; Y09392; CAA70559.1; -  
 DR EMBL; Y09392; CAA70560.1; -  
 DR EMBL; Y09392; CAA70561.1; -  
 DR EMBL; Y09392; CAA70562.1; -  
 DR EMBL; Y09392; CAA70563.1; -  
 DR EMBL; Y09392; CAA70564.1; -  
 DR EMBL; Y09392; CAA70565.1; -  
 DR EMBL; Y09392; CAA70566.1; -  
 DR EMBL; Y09392; CAA70567.1; -  
 DR EMBL; Y09392; CAA70568.1; -  
 DR EMBL; Y09392; CAA70569.1; -  
 DR EMBL; Y09392; CAA70570.1; -  
 DR EMBL; Y09392; CAA70571.1; -  
 DR EMBL; Y09392; CAA70572.1; -  
 DR EMBL; Y09392; CAA70573.1; -  
 DR EMBL; Y09392; CAA70574.1; -  
 DR EMBL; Y09392; CAA70575.1; -  
 DR EMBL; Y09392; CAA70576.1; -  
 DR EMBL; Y09392; CAA70577.1; -  
 DR EMBL; Y09392; CAA70578.1; -  
 DR EMBL; Y09392; CAA70579.1; -  
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 DR EMBL; Y09392; CAA70581.1; -  
 DR EMBL; Y09392; CAA70582.1; -  
 DR EMBL; Y09392; CAA70583.1; -  
 DR EMBL; Y09392; CAA70584.1; -  
 DR EMBL; Y09392; CAA70585.1; -  
 DR EMBL; Y09392; CAA70586.1; -  
 DR EMBL; Y09392; CAA70587.1; -  
 DR EMBL; Y09392; CAA70588.1; -  
 DR EMBL; Y09392; CAA70589.1; -  
 DR EMBL; Y09392; CAA70590.1; -  
 DR EMBL; Y09392; CAA70591.1; -  
 DR EMBL; Y09392; CAA70592.1; -  
 DR EMBL; Y09392; CAA70593.1; -  
 DR EMBL; Y09392; CAA70594.1; -  
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 DR EMBL; Y09392; CAA70599.1; -  
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 DR EMBL; Y09392; CAA70601.1; -  
 DR EMBL; Y09392; CAA70602.1; -  
 DR EMBL; Y09392; CAA70603.1; -  
 DR EMBL; Y09392; CAA70604.1; -  
 DR EMBL; Y09392; CAA70605.1; -  
 DR EMBL; Y09392; CAA70606.1; -  
 DR EMBL; Y09392; CAA70607.1; -  
 DR EMBL; Y09392; CAA70608.1; -  
 DR EMBL; Y09392; CAA70609.1; -  
 DR EMBL; Y09392; CAA70610.1; -  
 DR EMBL; Y09392; CAA70611.1; -  
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Cc 282 TQVPEQEMEVQ-----EPAEPGVNMLSPGES-----EHLLEPAEAEERSORRLVLP 328
Cc 265 PSSSEKICIVOLVGNWTFGYPETOALCPQVYWSMDQLPSRLALGPAAP-----TLSPE 319
Cc 329 ANEGDPTETLR---QCFFDPADLVPPDSWEPMLRKIGLMDNEITKAKAPAGHRDLYTM 385
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RESULT 7
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DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
GN (APO-1 ANTIGEN) (CD95 ANTIGEN).
OS TNERSF6 OR APT1 OR FAS OR FASL.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
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RN [1]
RP MEDLINE-91309137; PubMed-1713127;
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis."
RL Cell 66:233-243(1991).
RN [2]
RP MEDLINE-92268122; PubMed-1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen."
RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP STRUCTURE BY NMR OF 218-335.
RX MEDLINE-97122332; PubMed-8967952;
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Feelik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain."
RL Nature 384:638-641(1996).
Cc -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
Cc ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
Cc RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
Cc SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
Cc ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
Cc CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
Cc APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
Cc INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
Cc SUICIDE OF MATURE T-CELLS, OR BOTH.
Cc -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
Cc -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
Cc AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
Cc -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
Cc -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
Cc -1- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;

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Cc 282 TQVPEQEMEVQ-----EPAEPGVNMLSPGES-----EHLLEPAEAEERSORRLVLP 328
Cc 265 PSSSEKICIVOLVGNWTFGYPETOALCPQVYWSMDQLPSRLALGPAAP-----TLSPE 319
Cc 329 ANEGDPTETLR---QCFFDPADLVPPDSWEPMLRKIGLMDNEITKAKAPAGHRDLYTM 385
Cc 320 SPAGSPAMMLOPGPOLY-DVMDAVPARRWKEFVKTGLREAEIEAVEIGRFRDOQYEM 378
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Cc 379 LKRW--RQOQPAAGLGAVALERMG 401

RESULT 8
FASA_MOUSE STANDARD; PRT; 327 AA.
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AC P25446;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)

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WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".

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PIR: A40036; A40036.  
PIR: S24543; S24543.  
PDB: IDDE; 12-NOV-97.  
MIM: 134637; -  
InterPro: IPR000488; -  
InterPro: IPR001368; -  
Pfam: PF00020; TNFR\_c6; 2.  
Pfam: PF00531; death; 1.  
PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
PROSITE: PS50017; DEATH\_DOMAIN; 1.  
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
3D-structure.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 335 FASL RECEPTOR.  
FT DOMAIN 17 173 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 174 190 POTENTIAL.  
FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 47 166 3 X TNFR-CYS.  
FT REPEAT 47 83 TNFR-CYS 1.  
FT REPEAT 84 127 TNFR-CYS 2.  
FT REPEAT 128 166 TNFR-CYS 3.  
FT DOMAIN 230 314 DEATH DOMAIN.  
FT CARBOHYD 118 116 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 335 AA; 37732 MW; 0139942535111410 CRC64;

Query Match 8.5%; Score 197; DB 1; Length 335;  
Best Local Similarity 26.6%; Pred. No. 5.3e-07;  
Matches 77; Conservative 34; Mismatches 93; Indels 86; Gaps 14;

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Cc 38 LVIYVAIVL---VSAEALITOODLAPQOARAPQQRSSPSGL-----CPP 83
Cc 8 LPIVLISVARLSKSYNAQVTDINSKGL--ELRKVTYVETONLEGLHNDGFCRKP 65
Cc 84 GHH-----ISDGRDCISCKYGDVSTHMDLFLCRLCTCDGSG---EVELSPCTT 134
Cc 66 GERKAKDCTVNDDEPCVCGCEKKEYTDKAFHSSKRCRLCDEGHGLEVEIN-CT 124
Cc 135 TVCGCEEGTFREDDEPEMKRCRTGCPRGMAVVGCTPMSDIECYHKESGT----- 185
Cc 125 TWCRCRKNPFNCSTVCEHDCP--TKCEHGIIL--ECTLISNKC--KEGSSNIGWL 179
Cc 186 -----KHSGEPAVEETVTSPTPA-----SPCSLSGIIGIVTA 221
Cc 180 LLLPIPLIYVWRKVEYQKCRKHKRENGSHSPILNPETAIVAINISVDLSKYL-- 237
Cc 222 AVLLIYAVFVCKSLMKVLYPKIGICSGGGDPERVDSSQPGADNVLNIVSLQP 271
Cc 238 GVM-----TISQVKGFEVRKNGVNEAKIDEIK-----NDNV 267

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DE (APO-1 ANTIGEN) (CD95).  
GN TNFRSF6 OR APT1 OR FAS.  
OS Mus musculus (Mouse).  
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=92148151; PubMed=1371136;  
RX Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,  
RT Copeland N.G., Jenkins N.A., Nagata S.,  
RT "The cDNA structure, expression, and chromosomal assignment of the  
RT mouse Fas antigen."  
RL J. Immunol. 148:1274-1279(1992).  
RN [2]  
RP SEQUENCE OF 1-96 FROM N.A.  
RX MEDLINE=93189576; PubMed=7680478;  
RA Adachi M., Watanabe-Fukunaga R., Nagata S.,  
RT "Aberrant transcription caused by the insertion of an early  
RT transposable element in an intron of the Fas antigen gene of 1pr  
RT mice."  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).  
RN [3]  
RP VARIANT LPR.  
RX MEDLINE=92195401; PubMed=1372394;  
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,  
RA Nagata S.,  
RT "Lymphoproliferation disorder in mice explained by defects in Fas  
RT antigen that mediates apoptosis."  
RL Nature 356:314-317(1992).  
RN [4]  
RP FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
RX ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
RT RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
RT SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
RT ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
RT CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
RT APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
RT INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
RT SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
RN [5]  
RP TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,  
RX LIVER, LUNG, HEART, AND ADULT OVARY.  
RN [6]  
RP DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
RX AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
RN [7]  
RP DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION  
RX DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY  
RX PRODUCTION.  
RN [8]  
RP SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
RN [9]  
RP SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
RN [10]  
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RN [11]  
RX EMBL: M83649; AAA37593.1; -  
RX EMBL: S56490; AAB25700.1; -  
RX EMBL: S56485; AAB25700.1; JOINED.  
RX EMBL: S56486; AAB25700.1; JOINED.  
RX PIR: A66484; A66484.  
RX HSSP: P25445; 1DDF.  
RX MGD: MGI:95484; Fas.  
RX InterPro: IPR000488; -  
RX InterPro: IPR001368; -  
RX Pfam: PF00020; TNFR\_c6; 3.  
RX Pfam: PF00531; death; 1.  
RX PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
RX PROSITE: PS00650; TNFR\_NGFR\_2; 2.  
RX PROSITE: PS50017; DEATH\_DOMAIN; 1.  
RX Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;

KW Disease mutation. 21  
FT SIGNAL. 1  
FT CHAIN. 22 327  
FT DOMAIN. 22 169  
FT TRANSMEM. 170 186  
FT DOMAIN. 187 327  
FT DOMAIN. 43 162  
FT REPEAT. 43 79  
FT REPEAT. 80 123  
FT REPEAT. 124 162  
FT REPEAT. 222 306  
FT CARBOHYD. 43 43  
FT CARBOHYD. 114 44  
FT VARIANT. 246 246  
FT SEQUENCE. 327 AA; 37418 MW; F6BFFC3AC356EE CRC64;  
  
Query Match 7.7%; Score 179.5; DB 1; Length 327;  
Best Local Similarity 24.4%; Pred. No. 8.8e-06;  
Matches 87; Conservative 49; Mismatches 125; Indels 95; Gaps 20;  
  
QY 38 LVLYVAAVLLVSAESALITQDDLPQQRARPOQRKSSPSEGL-----CPRGHH 87  
DB 8 LPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNC--SEGLYGCGPPCCOPQPKKK 65  
QY 88 SEDGR-----DISCKYGQDY--STHMDLFLCLCTRCDSG---EVELSPCTTRNTY 136  
DB 66 VEDCKNKGTPTCAPCTEGKEVMDKNHYADK--CRCTLCDENHGLEVEN--CTLQNTK 122  
QY 137 CQCEGTFREEDSPENCRCRCRTGCPGMVAVGDCPTWSDIECVHKGSGTHSGEAPAVE 196  
DB 123 CKCKPFCYCSPCFCEHCVR--ASCENGTLE--PCTATSNIC--RKOS----- 165  
QY 197 TVYSSGTSPASPCSLGIIIGVAVVAVVAVFVC---KSLMKVLPYLKIGISGG 252  
DB 166 -----PNRMLTLTL-----VLLPLVFIYKRYKRCMR-----RQ 199  
QY 253 GDEYDRSSQSGADNVLEIVSLQTPQPE--QEMEVEPAPPTGYNMLSPSESR 310  
DB 200 DDE--SRSSRTTIMNMSNLSL-----KYPRIMEDIQAKKFARENNIKKEKIDE 253  
QY 311 LLEPAEARSQRR-RLLV---PANCDPTETL-----RQCDPDAVLVFPD 352  
DB 254 IMHDSIQDTAECKVQLLLWYQSHGKSDAYQDLIKGLKAKCAECRTLDKQDVMQKD 309  
  
RESULT 9  
FASA\_BOVIN STANDARD; PRT; 323 AA.  
AC P51867;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
CC (APO-1 ANTIGEN) (CD95).  
GN TNFRSF6 OR APT1 OR FAS.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96226401; PubMed=8634151;  
RX Yoo J., Stone R.T., Beattie C.W.,  
RT "Cloning and characterization of the bovine Fas."  
RL DNA Cell Biol. 15:227-234(1996).  
RN [2]  
RP FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
RX ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
RX RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
RX SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
RX ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
RX CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING

CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL, U34794; AAC48546.1; -.  
 CC HSSP; P25445; 1DDF.  
 CC InterPro: IPR000488; -.  
 CC InterPro: IPR001368; -.  
 CC Pfam: PF00020; TNFR\_C6; 3.  
 CC Pfam: PF00531; death\_1.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 CC PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 CC K0 Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.  
 CC FT SIGNAL 1 16 POTENTIAL.  
 CC FT CHAIN 17 323 FAST RECEPTOR.  
 CC FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 171 188 POTENTIAL.  
 CC FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 45 163 3 X TNFR-CYS.  
 CC FT REPEAT 45 80 TNFR-CYS 1.  
 CC FT REPEAT 81 124 TNFR-CYS 2.  
 CC FT REPEAT 125 163 TNFR-CYS 3.  
 CC FT DOMAIN 238 306 DEATH DOMAIN.  
 CC SO SEQUENCE 323 AA; 36445 MW; 4D8BA90E9E1F4892 CRC64;  
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 CC Query Match 7.6%; Score 176.5; DB 1; Length 323;  
 CC Best Local Similarity 26.8%; Pred. No. 1.4e-05;  
 CC Matches 68; Conservative 35; Mismatches 88; Indels 63; Gaps 14;  
 CC  
 CC QY 74 SSPSEGL-----PPGHHSIEDGR-----DCISCKYGDYS--THNNDLFLCLR 115  
 CC Db 43 NSCGGLVREHFOCCGPPKRRKNGDCKRODTPCYVLCSSGNETYDKSHSDK--CIR 100  
 CC QY 116 CTRCDG---EYELSPCTTNTNTVCOCCEGTFREEDSPKCRKRTGCPRGWVKGDCIP 172  
 CC Db 101 CSICDEHGLEVEON-CTRTNTKCRCKSNFPCNSPCHNCPTT-CENGLIE--KCTP 156  
 CC QY 173 WSDICVAKESGKTSKSGEAPVEETVTSPPGSPASCSGIIIGVTVAAVLIYAVFPC 232  
 CC Db 157 TSNKYC-----KGRSHANSIMALLI--LLPIVLII-YKVV 190  
 CC QY 233 KSLMKKVLPLKLGICSGGG---DPERVDRSSQRP-AEDVNLVEIYSIIPTQVPEGE 288  
 CC Db 191 KSREKTKNDYCNASASNDGRLNLTVDDGKYLPSIAEQRIEVEVEFKNMEEK 250  
 CC QY 289 ME-----VQEPAE 296  
 CC Db 251 IDDIMHDVHETAE 264  
 CC  
 CC RESULT 10  
 CC TNRL\_RAT STANDARD; PRT; 461 AA.  
 CC ID TNRL\_RAT  
 CC AC P22934;  
 CC DT 01-AUG-1991 (Rel. 19, Created)  
 CC DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 CC DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)

DE (P35).  
 CC TNFRSF1A OR TNFR1 OR TNFR-1.  
 CC OS Rattus norvegicus (Rat).  
 CC CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_Taxid=10116;  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=91090841; PubMed=1702293;  
 CC RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheinrich P., Pfizenmaier K.,  
 CC Lantz M., Olsson I., Hauptmann R., Stratawa C., Adolf G.R.,  
 CC "Molecular cloning and expression of human and rat tumor necrosis  
 CC factor receptor chain (p60) and its soluble derivative, tumor  
 CC necrosis factor-binding protein.";  
 CC RL DNA Cell Biol. 9:705-715(1990).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL, M63122; AAA42256.1; -.  
 CC PIR; B36555; B36555.  
 CC HSSP; P19438; 1TNR.  
 CC InterPro: IPR000488; -.  
 CC InterPro: IPR001368; -.  
 CC Pfam: PF00020; TNFR\_C6; 4.  
 CC Pfam: PF00531; death\_1.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 CC PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 CC K0 Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
 CC FT SIGNAL 1 21 POTENTIAL.  
 CC FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 CC FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 212 234 POTENTIAL.  
 CC FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 43 196 4 X TNFR-CYS.  
 CC FT REPEAT 43 82 TNFR-CYS 1.  
 CC FT REPEAT 83 125 TNFR-CYS 2.  
 CC FT REPEAT 126 166 TNFR-CYS 3.  
 CC FT REPEAT 167 196 TNFR-CYS 4.  
 CC FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).  
 CC FT DOMAIN 363 448 DEATH DOMAIN.  
 CC FT DISULFD 44 58 BY SIMILARITY.  
 CC FT DISULFD 59 72 BY SIMILARITY.  
 CC FT DISULFD 62 81 BY SIMILARITY.  
 CC FT DISULFD 84 99 BY SIMILARITY.  
 CC FT DISULFD 102 117 BY SIMILARITY.  
 CC FT DISULFD 105 125 BY SIMILARITY.  
 CC FT DISULFD 127 143 BY SIMILARITY.  
 CC FT DISULFD 146 158 BY SIMILARITY.  
 CC FT DISULFD 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 461 AA: 50969 MW: EB23C05450FB202 CRC64;

Query Match 7.58; Score 173.5; DB 1: Length 461;  
 Best Local Similarity 21.48; Pred. No. 3.5e-05;  
 Matches 107; Conservative 53; Mismatches 168; Indels 171; Gaps 25;

QY 32 PRPKTLVVAVALLL--VSAESALI-TQODLAPQOARAPQKRSPSEG-----LCP 82  
 DB 4 PIVPGLLSLVLLALMGHPGVTGLVPSLGRKRDNLCPGKTAHPNNSICTCKH 63  
 QY 83 PGHNSID--GRD--CISCKYGDYSTMNDLFLCLRCTRC--DSGEVLSPTTTRN 134  
 DB 64 KGTLYVSDPSPGQETVCEYCDKG-TFTASQNHVROCLSCCKRKEMFQVEISPKADM 122  
 QY 135 TVQOCSEGTFR--EDSPKCRKCRGCPRGKVV-----GDCTP 172  
 DB 123 TVGCKKNOFORVLSHFQCVDC-SPCFNGTVTIPCKEKONTVCNCHAGFLSGNECTP 181  
 QY 173 WSDIECVHKSSTKHSSEA-----PAVEETVSSPTGPAFSLGIIIGTVAAVLI 226  
 DB 182 -----CSH-----CKNDECKKLLPRVANTNPQDST-----AVLLPIVFLGLC 223  
 QY 227 VAVFVCKSL--WKVLPYLKIGCSGGGDPERVYRASSRPGAEVDVNLNIVSLQP 281  
 DB 224 LLEFICISILCRPQW-----RP-----RVYSITCR 249  
 QY 282 TVPQEDME-----VOEPAETGVNMLSPG-----SHLLPRAEAE 319  
 DB 250 DSAPVKEVEEGIVTKPLRPASIPAFSPNPGFNPLGFTTPRFSHPVSSTPSVFGPS 309  
 QY 320 SQRR-----RLVAVANEGD-----TEFLROCFDFA----- 346  
 DB 310 NMHNPVPVPEVPTGADPLLYGSLNPVPIPAVKKEVVAOORLDTADPAMLYAV 369  
 QY 347 -DLVPEDSMELRKLGMLDNEI-KVAKAEAGHRDLYTMLIKWNKTR-----DASY 399  
 DB 370 VDGVPPTPKMEFRLLGSLSHETRELQNGRCRLREAHYMLEAMRRRTFRHEATLDVVG 429  
 QY 400 HTLLD-----ALETLGERL 413  
 DB 430 RVLCDMNLRCLENIREFTL 448

RESULT 11  
 TNR2\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
 BINDING PROTEIN 2) (TNFRI) (P80) (TNF-R2) (CD120B) (ETANERCEPT).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 OX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; Pubmed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G., Solam L., Beckmann M.P., Jerzy R.,  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=9104591; Pubmed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vanlice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; Pubmed=8661109;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RN [4]  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; Pubmed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN [5]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; Pubmed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [6]  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; Pubmed=2173696;  
 RA Loetscher H., Schlaepper E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brocksch W.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from Hs60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [7]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016040; Pubmed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.  
 RX MEDLINE=99221490; Pubmed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC WYETH-AVERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMIGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNF-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/";  
 CC -1-  
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DR EMBL: M32315; AAA59929.1; -  
DR EMBL: M35857; AAA63262.1; -  
DR EMBL: U52165; AAC50622.1; -  
DR EMBL: U52156; AAC50622.1; JOINED.  
DR EMBL: U52157; AAC50622.1; JOINED.  
DR EMBL: U52158; AAC50622.1; JOINED.  
DR EMBL: U52159; AAC50622.1; JOINED.  
DR EMBL: U52160; AAC50622.1; JOINED.  
DR EMBL: U52161; AAC50622.1; JOINED.  
DR EMBL: U52162; AAC50622.1; JOINED.  
DR EMBL: U52163; AAC50622.1; JOINED.  
DR EMBL: U52164; AAC50622.1; JOINED.  
DR EMBL: M55994; AAA36755.1; -  
DR PIR: A35356; A35356.  
DR PIR: A36007; A36007.  
DR PIR: A36475; A36475.  
DR PIR: B35010; B35010.  
DR PIR: A23666; A23666.  
DR PDB: 1CA9; 12-Apr-99.  
DR MIM: 191191; -  
DR InterPro: IPR001368; -  
DR Pfam: PF00020; TNFR\_C6; 4.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
KW Phosphorylation; Pharmaceutical; 3D-structure.  
FT SIGNAL 1 22  
FT CHAIN 1 461  
FT DOMAIN 23 257 TUMOR NECROSIS FACTOR RECEPTOR 2.  
FT TRASMEN 258 287 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 288 461 POTENTIAL.  
FT DOMAIN 39 201 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 39 76 4 x TNFR-CYS.  
FT REPEAT 77 118 TNFR-CYS 1.  
FT REPEAT 119 162 TNFR-CYS 2.  
FT REPEAT 163 201 TNFR-CYS 3.  
FT DISULFID 40 53 TNFR-CYS 4.  
FT DISULFID 54 67 BY SIMILARITY.  
FT DISULFID 57 75 BY SIMILARITY.  
FT DISULFID 78 93 BY SIMILARITY.  
FT DISULFID 96 110 BY SIMILARITY.  
FT DISULFID 100 118 BY SIMILARITY.  
FT DISULFID 120 126 BY SIMILARITY.  
FT DISULFID 134 143 BY SIMILARITY.  
FT DISULFID 137 161 BY SIMILARITY.  
FT CARBOHYD 164 179 BY SIMILARITY.  
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 141 141 R -> P (IN REF. 4).  
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
FT CONFLICT 363 363 A -> T (IN REF. 4).  
FT SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

Query Match 7.4%; Score 172; DB 1; Length 461;  
Best Local Similarity 22.4%; Pred. No. 4,4e-05;  
Matches 88; Conservative 40; Mismatches 134; Indels 130; Gaps 17;

OY 81 CPGHH-----ISEGRCISCKYGADYSTHNDLLFCILRC-TRDCSGVELSPCTTRTN 134  
DB 57 CSPGHAVVFCFKTSDYCDSE-DSTYTQLMNWPPELISCSGSSDQVEQACTRDN 115  
OY 135 TVCQCEBETFEEDSPENC-----RKCRTCPRGMVAVGDTCPMSDIECVHKESGT--- 185  
DB 116 RICRCPGMYCALSKQECGRICAPLRKCRPGF--GVARRG--TETSDVVCPCAGTSTN 171  
OY 186 -----KHSGEAP 192

DB 172 TRSSTICRPHQICNVVAIPGNASRDVCTSTPSRSMAPGVHLDPYSTSSQHTQPTP 231  
OY 193 ABEETVSS--PGTPASPCSS-----GIIGVVAAVVLIYAVVC--KSLMKK 239  
DB 232 EPSTASTSTFLPMGSPSPAECSGTGFALPGLYGVLT-ALGLLIGVNCVIMQVKK 290  
OY 240 VL-----PYLKGICSGGGDDPREVDSSORPQAEVNLVEIYSILO--PTQPEQE 288  
DB 291 PCLQREARVPHLPADKAGTQGPQOHLITAPSSSSSSLSASALDRAPTRNQPQA 350  
OY 289 MEVO-----EPAETGVNMLSPC-----ESEHLEPAEASRRRLIV 327  
DB 351 PVEAGAGAEARASTSSSPSGGHGTQVNVCIYVNCSSDH-----SSQCSSASTM 405  
OY 328 PANEGDPTETLRQCPDDPADLVFPDSWEPLMR 359  
DB 406 GPTDSSPSESPPD-----EOVPFSKECAFR 431

## RESULT 12

FASTA\_PIG STANDARD; PRT; 332 AA.  
AC 077736;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
DE (APO-1 ANTIGEN) (CD95).  
GN TNFRSF6 OR APR1 OR FAS.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_Taxid=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
RT \*Expression of apoptosis-associated genes in hibernating and stunned  
RT myocardium of pig.\*;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC  
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DR EMBL: AJ001202; CA04596.1; -  
DR InterPro: IPR000488; -  
DR InterPro: IPR001368; -  
DR Pfam: PF00020; TNFR\_C6; 3.  
DR Pfam: PF00531; death; 1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.  
FT SIGNAL 1 16 POTENTIAL.



DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 01-OCT-2000 (Rel. 40, last annotation update)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LINGFR) (P75 ICD).  
 GN NGFR OR TNFRSF16.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87051725; PubMed=3022937;  
 RA Johnson D., Iannahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,  
 RA Bothwell M., Chao M.;  
 RL "Expression and structure of the human NGF receptor.";  
 RL Cell 47:545-554(1986).  
 RL [2]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=89096903; PubMed=2850481;  
 RA Sehgal A., Patil N., Chao M.;  
 RL "A constitutive promoter directs expression of the nerve growth factor  
 receptor gene.";  
 RL Mol. Cell. Biol. 8:3160-3167(1988).  
 RT -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 RT NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: M14764; AAB59544.1; -  
 DR EMBL: M21621; AAA36363.1; -  
 DR PIR: A23218; GOHON.  
 DR HSP: P07174; INGR.  
 DR MIM: 162010; -  
 DR InterPro: IPR000488; -  
 DR InterPro: IPR001368; -  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR Pfam: PF00531; death; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_2; 4.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;  
 KW phosphorylation; Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 427  
 FT DOMAIN 29 250 LOW-AFFINITY NERVE GROWTH FACTOR  
 FT TRANSMEM 251 272 RECEPTOR.  
 FT DOMAIN 273 427 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 31 189 POTENTIAL.  
 FT REPEAT 31 65 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 66 107 4 X TNFR-CYS.  
 FT REPEAT 108 147 TNFR-CYS 1.  
 FT REPEAT 148 189 TNFR-CYS 2.  
 FT REPEAT 189 421 TNFR-CYS 3.  
 FT DOMAIN 344 421 TNFR-CYS 4.  
 FT DISULFID 32 43 DEATH DOMAIN.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 89 107 BY SIMILARITY.

FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT CARBOHYD 60 60 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64.  
 Query Match 7.1%; Score 166; DB 1; Length 427;  
 Best Local Similarity 20.0%; Pred. No. 0.00011;  
 Matches 98; Conservative 54; Mismatches 167; Indels 170; Gaps 20;  
 QY 28 ARGPVPRKTVLVVAANVLLVSAESALITQODLAPQORAPQORSSPSBGLCPGHHI 87  
 DB 9 AMGPRLILLLLLGVS---LGAKAE-----CPTGLY- 37  
 OY 88 SEDGRDCISCKYGODY-----STHMNDLF---CLRCTDSEVELS 127  
 DB 38 THSGECKKACNMGEGVADPCGANOTVCEPCLDSTVFSVATPECKPCTECVGLQSKSA 97  
 OY 128 PCTTRNTVCOCEGTFREEDSP--EMCRKCRTG-----CPRGMV--- 165  
 DB 98 PCVEADDAVCRCAYGYODETTCGCEACRCVCGSLVFCODKONTVCEPCPDGTYSDE 157  
 OY 166-----KVGDCTPMSDIECH-----KESGRHSGEA 191  
 DB 158 ANHVDPCLCPTVCEPTREQLRECTRMADAECIEIPGRMITSREPGSDSTAPSTQDEEA 217  
 OY 192 PAVEETVTSPP-----TPASPSLSGIITGVAAVVLIVAVFCKSLW 237  
 DB 218 PEGDLIASTVAGVYTTWSSQPVYTGTDNLIPVCSILAAVYGLVAFKR--W 275  
 OY 238 KAVLPYLKIGICSGGDDPERDRSSORPGAEVDNVLNIVLSILOPTQVPEQMEVQEPAP 297  
 DB 276 NS---CKQNKQGANSRP-----VNOTPPPEGEKIHSDSGI---SVDSQSLHQQPHQTQ 322  
 OY 298 T--GYNMLSPGSEHLLPFAERERQRRLLVPAENGPTELTQCFDFADYLPFDSME 355  
 DB 323 TASGQALGGDGLYSSLPAPAREVEK---LINGSAG-----DTRW 360  
 OY 356 PLMRILGLMNDNEIKYAKAEAGHRDTLYTMLIKWNKTRGDSAVHTLDALETGERLAK 415  
 DB 361 HLAGLGQYPERHDSFTHEACPVR---ALLASWA--TQDSATIDALLAL---RRIQR 410  
 OY 416 QKIDPHLS 424  
 DB 411 ADLVESLCS 419  
 RESULT 15  
 TNR2\_MOUSE STANDARD; PRT; 474 AA.  
 ID TNR2\_MOUSE  
 AC P25119; P97893;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).  
 GN TNFRSF1B OR TNFR2 OR TNFR-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9118785; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.;  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";





